

Figure 1

Gene and AA sequence

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      M L G K F S Q T C Y N S A I Q G S V L T S T C E R T N G G
1 AGGAGGACAG CTATGCTGGG CAAGTTCAGC CAGACCTGCT ACACAGCGC GATTCAGGCG AGCGTTCTGA CCAGCACCTG CGAACGTACC AATGGTGGCT
  TCCTCCTGTC GATACGACCC GTTCAAGTCG GTCTGACGCA TGTGTGCGG CTAAGTCCCG TCGCAAGACT GGTGCTGGAC GCTTGCATGG TTACCACCGA

      Y N T S S I D L N S V I E N V D G S L K W Q P S N F I E T C R N T Q
101 ACAACACTTC TAGCATTCAT CTGAACAGCG TGATTGAGAA TGTGGATGGC TCTCTGAAT GGCAGCCGAG CAACTTCATT GAAACCTGTC GCAACACCCA
  TGTGTGAAG ATCGTAAC TAACCTGTCG ACTAATCTTT ACACCTACCG AGAGACTTTA CCGTCGGCTC GTTGAAGTAA CTTTGGACAG CGTTGTGGGT

      L A G S S E L A A E C K T R A Q O F V S T K I N L D D H I A N I D
201 GCTGGCGGCG AGCTCTGAAC TGGCGGCAGA ATGCAAGACT CGCGCGCAGC AGTTTGTGAG CACCAAGATC AACCTGGACG ATCACATCGC GAACATTCAT
  CGACCGCCCG TCGAGACTTG ACCGCCGTCT TACGTTCTGA GCGCGCGTCG TCAAACTC GTGGTCTAG TTGGACCTGC TAGTGTAGCG CTTGTAACTA

      G T L K Y E #
301 GGCACCCCTGA AGTATGAATA A
  CCGTGGGACT TCATACTTAT T

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Figure 2

AA alignment

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.....LGKFSQTCYN SAIQGSVLTSTCERTNGGYNTSSIDLNSVIENV DGLKWP SNFI 55
|||||
MLGKFSQTCYN SAIQGSVLTSTCERTNGGYNTSSIDLNSVIENV DGLKWP SNFI 56

ETCRNTQLAGSSELAAECKTRAQQFVSTKINLDDHIANIDGTLKYE* 101
|||||
ETCRNTQLAGSSELAAECKTRAQQFVSTKINLDDHIANIDGTLKYE* 102

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Figure 3

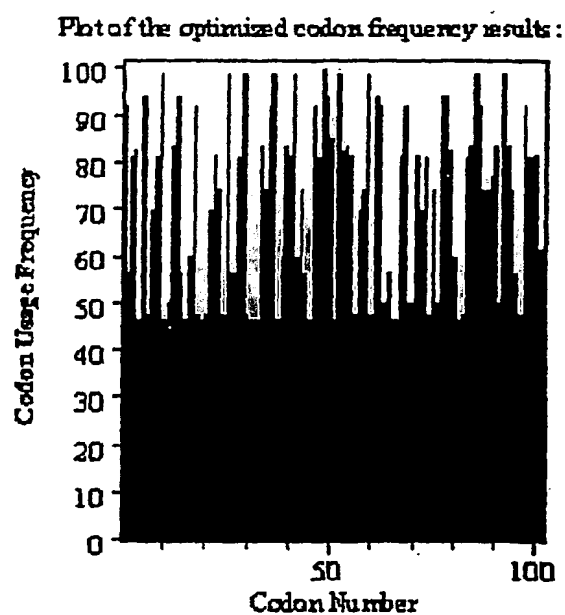


Figure 4

1 atccggatat agttcctcct ttacgcaaaa aacccctcaa gaccctgita gaggcccaa
 61 ggggttatgc tagtatgc tcagcgggtg cagcagccaa ctacgttcc ttccgggt
 121 tgitagcagc cggatcagc tgggtgggtt ggtgggtc gacatcccg gggcttccg
 181 gggcgagttc tggctggcta gcccgttga tctcaggtt ttcatatc aggtgcca
 241 caatgtcgc gatgtatc tccaggtga tcttgggt cacaactgc tgcgcggag
 301 tctgcatc tgcgcgagc tcagagctc cgcgcagct ggtgttgc caggttcaa
 361 tgaagtgtt cggctgcat ttacagagc catccatc ctcacacg ctgtcagat
 421 caatgtcaga aggtgtgag caaccatgg tccgttgc ggtgtgtc agaacgtgc
 481 cctgaatgc gctgtgtg caggtctggc tgaactgcc caggtatgt atactcct
 541 cttaagta acaaaaatta ttctagagg ggaattgta tccgtcaca attccctat
 601 agtgagctgt attaatctc cgggatcag atctcgtcc tctacgccg acgcatcgt
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 841 gcggcggtgc tcaacggcct caacctacta ctgggtgct tctaatgca ggagtgc
 901 aaggagagc gtcgagatc cggacacat cgaatggcg aaaaccttc gcggtatgg
 961 atgatagcg cgggaagaga gtcaattcag ggtggtgaat gtgaaccag taacgtata
 1021 cgatgtcga gatatgccg gtgtctctta tcagacggt tcccgttg tgaaccagg
 1081 cagccaggtt tctcgaaaa cgcgggaaa agtggagcg gcgatggcg agctgaatta
 1141 cattccaac cgtgtggc acaactggc gggcaaacag tctgtctga ttggcgtgc
 1201 cactccagt ctggccctgc acgcgccgt cgaattgtc gcggcgatta aatctcgcg
 1261 cgatcaactg ggtgccagcg tgggtgtgc gatgtagaa cgaagcgcg tgaagcctg
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 1801 tatctcgga tgggatac agataccga agacagctc tttatatc cccgttaac
 1861 caccatcaa caggatttc gcctgtctgg gcaaacagc tggaccgct tctgcaact
 1921 ctctcaggg caggcggtga agggcaatc cgtgttccc gctcactg tgaagagaaa
 1981 aaccacctg gcgccaata cgaaacgc ctctcccg cgttggcg attcataat
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Figure 4 (Continued)

3001 tctgtgaatc gcttcacgac cacgctgatg agcttiaccg cagctgcctc gcgcgtttcg
 3061 gtgatgacgg tgaataacctc tgacacatgc agctcccga gacgggcaca gcttgtctgt
 3121 aagcggatgc cgggagcaga caagcccgtc agggcgcgtc agcgggtgtt ggccgggtgc
 3181 ggggcgcagc catgaccagc tcacgtagcg atagcggagt gtatactggc ttaactatgc
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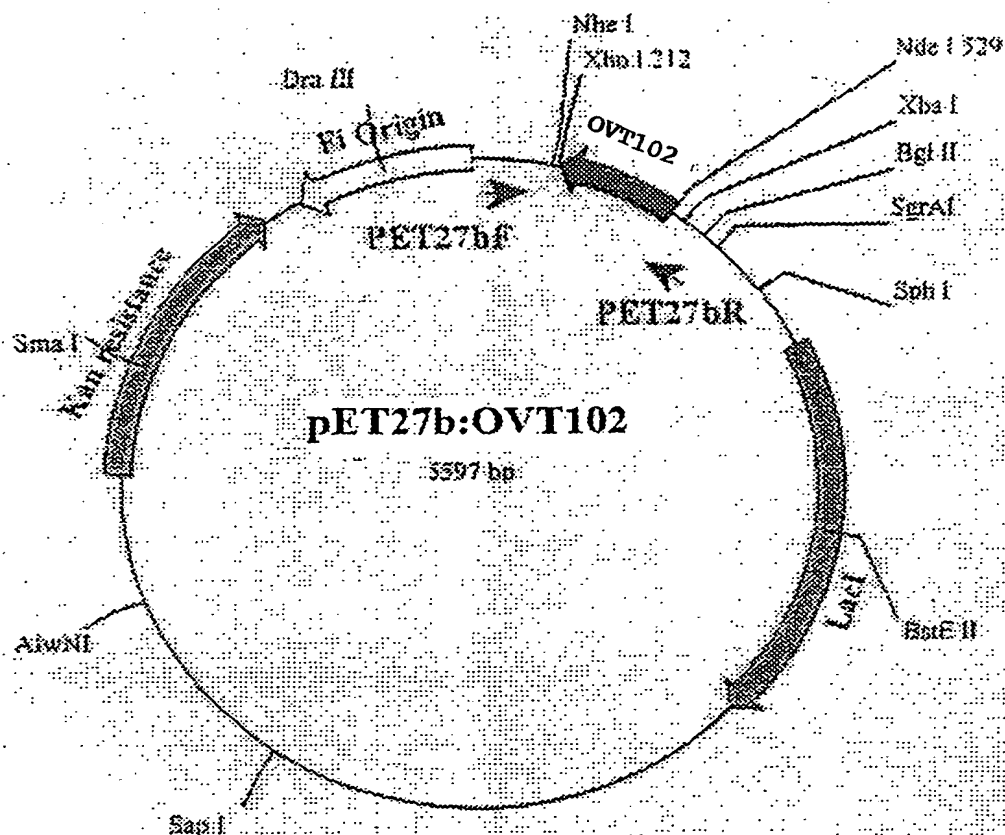
Figure 5

FIGURE 6



1 2 3 4 5 6 7 8 9 10 11 12

FIGURE 7

